Interpreting Evolutionary Diagrams: When Topology and Process Conflict

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Abstract: The authors argue that some diagrams in biology textbooks and the popular press presented as depicting evolutionary relationships suggest an inappropriate (anagenic) conception of evolutionary history. The goal of this research was to provide baseline data that begin to document how college students conceptualize the evolutionary relationships depicted in such noncladogenic diagrams and how they think about the underlying evolutionary processes. Study 1 investigated how students ($n = 50$) interpreted the evolutionary relationships depicted in four such evolutionary diagrams. In Study 2, new students ($n = 62$) were asked to interpret what the students in Study 1 meant when they used the terms *evolved into/from* and *ancestor/descendant of*. The results show the interpretations fell broadly into two categories: (a) evolution as an anagenic rather than cladogenic process, and (b) evolution as a teleological (purpose-driven) process. These results imply that noncladogenic diagrams are inappropriate for use in evolution education because they lead to the misinterpretation of many evolutionary processes. © 2010 Wiley Periodicals, Inc. J Res Sci Teach 47: 861–882, 2010
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Despite the fact that evolution underpins understanding in all the life sciences and should be a major element of general science literacy, alternative conceptions, and knowledge deficits persist. The newly revitalized push for enhanced public understanding of science makes it timely to consider the effectiveness of contemporary evolution curricula. A comprehensive evolution curriculum should include at least the following components: common ancestry, variation, homology, natural selection, and speciation. Indeed, the codes that emerged from the Study 1 analyses provide strong support that these critical components do in fact underpin an understanding of evolution. And in a perfect world such a curriculum would combine microevolution with macroevolution to provide comprehensive understanding of the full sweep of evolutionary processes and patterns (Catley, 2006).

Much recent research on evolution education has primarily considered students' and teachers' attitudes towards and acceptance of the theory of evolution (e.g., Deniz, Donnelly, & Yilmaz, 2008; Donnelly & Boone, 2007; Poling & Evans, 2004), as well as the effects of teachers' attitudes on their teaching (e.g., Goldston & Kyzer, 2009). Microevolution has been the primary content focus, with studies investigating students' understanding of natural selection (e.g., Anderson, Fisher, & Norman, 2002; Nehm & Schonfeld, 2008) and methods for teaching natural selection (e.g., Passmore & Stewart, 2002; Sandoval & Reiser, 2003). Additional research has considered students' understanding of evolution more generally (e.g., Shtulman, 2006), including a focus on the role conceptual change plays in students' understanding of evolutionary processes (e.g., see Treagust & Duit, 2008).

Recently, a number of researchers have called for the inclusion of macroevolutionary concepts in evolution education (e.g., Baum, Smith, & Donovan, 2005; Catley, 2006; Catley, Lehrer, & Reiser, 2005), an

area that is typically poorly taught and woefully underrepresented in the research literature. This is the topic we examine in the present research. Understanding macroevolution implies understanding evolutionary history. Hypotheses about evolutionary history are generally depicted in phylogenetic diagrams, which represent patterns of evolutionary relationships among taxa that provide a framework to help people think about processes that might account for these patterns (e.g., Clark, 2001; Gould, 1995). It is critical to investigate how students understand the information depicted in phylogenies as a prelude to teaching them how to interpret and reason from such diagrams.

One of the earliest phylogenetic depictions is of the Great Chain of Being. This far-reaching concept, rooted in the ideas of Plato and Aristotle, encompasses the physical and metaphysical world in an unbroken chain that stretches from nonliving matter to supernatural beings. This Chain and the ideas it embodies are important in understanding the underpinnings of many evolutionary diagrams. It is possible to trace a connection from the Great Chain of Being depicted in Didacus Valades' 1579 *Rhetorica Christiana* (Lovejoy, 1936), through Bonnet's (1745) Scala Naturae (scale of being) which first elaborated these ideas in biology, then to Lamarck's (1809) extension of the ''chain'' in *Philosophie Zoologique*, and, finally, to Darwin's (1858) phylogeny in the *Origin of Species* and Haeckel's trees of the late 1800s (e.g., see Figure 1).

Diagrams containing elements of these historic visualizations remain prevalent today both in the popular arena (e.g., media depictions of evolution) and in science education (e.g., biology textbooks). Catley and Novick (2008) found that textbooks ranging from middle school to upper level college present a range of evolutionary diagrams. Some of these diagrams illustrate what is known about macroevolutionary theory more robustly than others. In particular, cladograms convey patterns of nested sets of taxa supported by *most recent common ancestors* (MRCAs—the most recent taxon from which all taxa in the group are directly descended) and suggest that speciation is a process of cladogenesis (a population of one species splitting into two). Noncladogenic diagrams, on the other hand, do not illustrate such nested sets of taxa and are ambiguous as to whether speciation events were the result of anagenesis (one species evolving directly into another) or cladogenesis. These latter diagrams are especially prevalent in high school textbooks (47% of all evolutionary diagrams) and in college textbooks geared toward introductory biology classes for nonmajors (35% of all evolutionary diagrams).

Although a few papers have presented data on students' interpretations of cladograms (Meir, Perry, Herron, & Kingsolver, 2007; Novick & Catley, 2010; Sandvik, 2008), to the best of our knowledge there is no literature on students' interpretations of noncladogenic evolutionary diagrams. Determining how students understand the nature of evolutionary relationships depicted in such diagrams is critical for ascertaining how best to prepare students to reason with scientifically valid diagrams (cladograms) and for bringing the teaching of macroevolution on par with microevolution in our schools. Catley and Novick (2008) suggested that scientifically inaccurate diagrams may be less effective for instruction and may contribute to misunderstandings of macroevolutionary theory. The two studies reported here provide support for this contention.

A Brief Synopsis of Modern Evolutionary Thinking

Modern understanding of speciation events suggests that new species are formed when the population of a parent species is fragmented (e.g., due to a geological barrier), and selection continues separately in each group, driven by pressures of the local environment. The resultant traits, when fixed in each sub-population, become the characters that are the markers of the speciation event itself.

Monophyletic groups (also called clades) are based on the concept of synapomorphies (shared, derived characters) that define hierarchically nested sets of taxa (or clades) that have been generated by a series of branching events. Such groups contain an ancestor and all of its descendents and are supported by special characters called synapomorphies. Modern disciplinary practice reconstructs these natural (or monophyletic) groups utilizing cladistic methodology (Catley, 2006; Hennig, 1966) and presents the results as phylogenies in the form of cladograms. For example, Figure 2 provides a cladogenic view of the evolutionary relationships among selected taxa in Haeckel's tree shown in Figure 1.

The perspective provided by cladograms is in sharp contrast to the approach portrayed in many diagrams—those used in the present research in particular—that often place taxa in an ordered linear progression suggesting anagenesis. Anagenesis is a process whereby one species evolves directly into
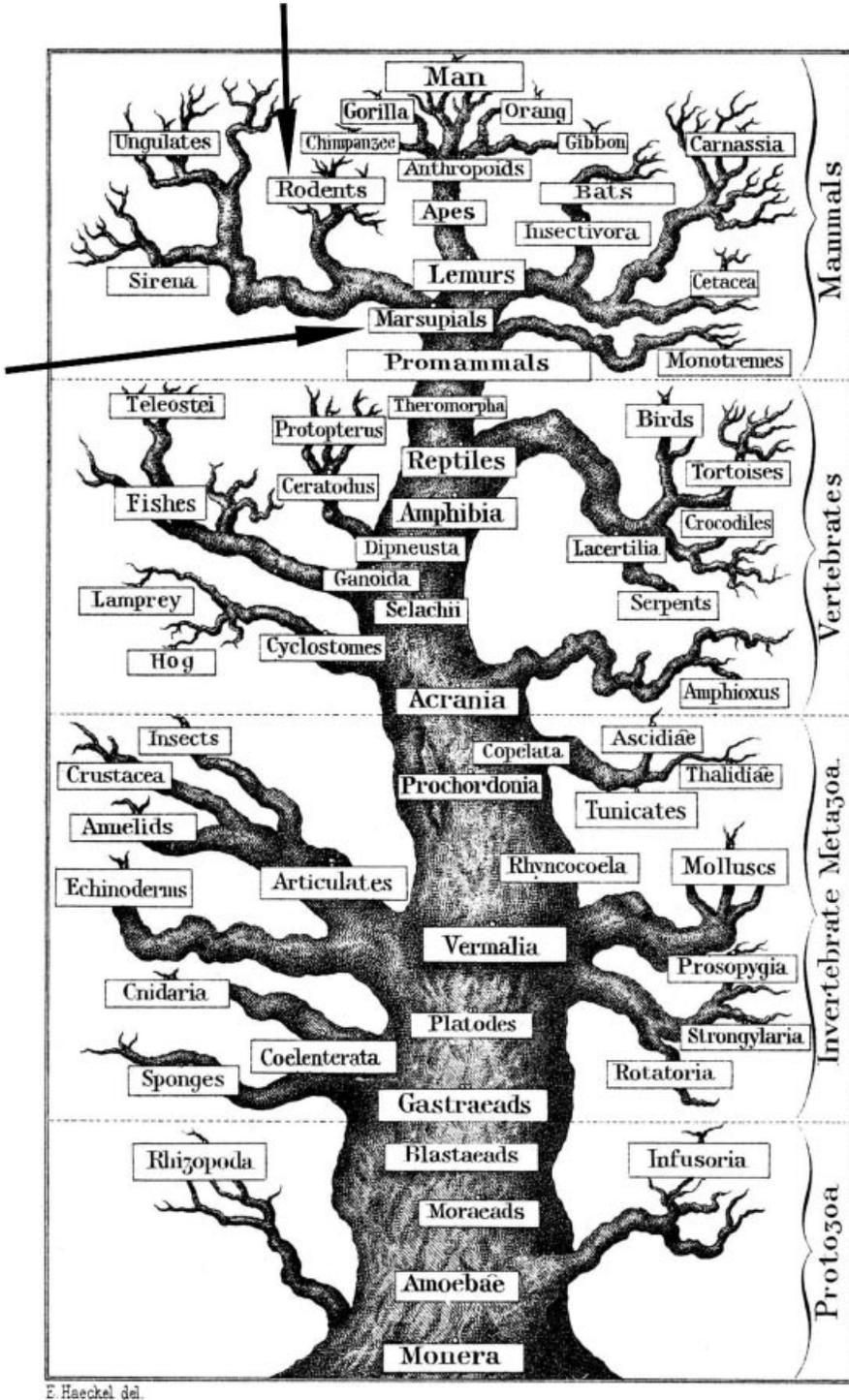
Figure 1. Haeckel's tree of life adapted from http://www.stclairresearch.com/content/historyDNA.html. This diagram is not a cladogram.
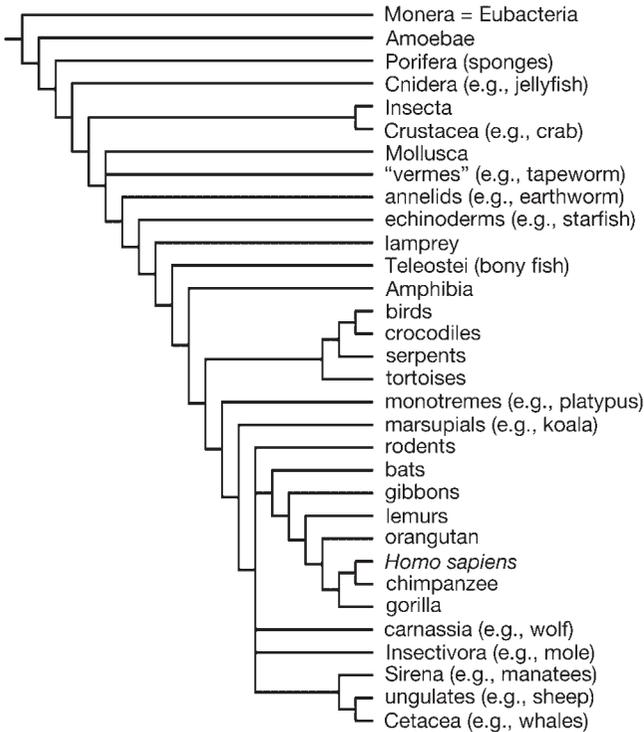
Figure 2. A cladogram representing modern understanding of the evolutionary relationships among selected taxa in Figure 1—Haeckel's tree of life. (Relationships are based on those from The Tree of Life web project 2005: http://tolweb.org/tree/phylogeny.html.)

another without any branching events. Cladogenesis, in contrast, is a process whereby a population of one species splits into two by the processes of speciation noted earlier.

Although change within a single species is well documented, one species changing into another species is not. Diversification and radiation of species within clades can only be achieved by branching or cladogenic events. If new species only arose by anagenesis, then there would never be a net increase in the total number of species. The fossil record provides no evidence to support such a contention.

Justification for Our Research

In the past two decades, there have been calls for efforts to enhance the efficacy of, and increase the opportunity for, tree thinking in life science education (e.g., Baum et al., 2005; Catley, 2006; Catley et al., 2005; O'Hara, 1988)—that is, an approach to teaching evolution based on cladogenic representations. Since the early 1990s, cladograms and phylogenetic theory have begun to appear in introductory biology texts (e.g., Starr & Taggart, 1992). However, treatments continue to be confined to its use in classification (e.g., Audesirk, Audesirk, & Byers, 2004; see Catley & Novick, 2008, for a review).

Despite the calls for a tree-thinking approach in evolution education and the appearance of branching phylogenetic trees in modern textbooks, students are still exposed to evolutionary diagrams other than cladograms in their biology textbooks, the popular media, and, sometimes, the scientific press. We sought to determine whether the information students extract from noncladogenic diagrams is in accordance with contemporary understanding of evolutionary theory/mechanisms.

Overview of Our Studies

In Study 1, we examined university students' interpretations of the evolutionary relationships among taxa depicted in a variety of noncladogenic evolutionary diagrams. We expected that the linear depictions of evolutionary history contained in these diagrams might lead students to provide explanations consistent with an anagenic rather than a cladogenic interpretation of evolutionary history—for example, of *H. habilis*

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changing into *H. sapiens* over time. In a recent study of students' reasoning about evolutionary relationships depicted in cladograms, Novick and Catley (2010) found that subjects provided anagenic interpretations of evolutionary history too infrequently to require coding. Because the students in that study were recruited from the same university as the students who participated in the present research, if anagenic interpretations are found in this study, we feel confident in concluding that they were a function of the information provided in the diagrams. Clearly it is not the case that students provide anagenic responses to evolutionary relationship questions regardless of the type of diagrammatic evidence they are given to evaluate.

To clarify the explanations students in Study 1 gave to support their interpretations, we conducted a second study examining students' understanding of particular terms used to describe evolutionary relationships. Because students were asked about the meanings of particular evolutionary terms, we expected we might see evidence of other alternative conceptions of evolution in addition to anagenesis. In particular, we expected we might see evidence of teleological thinking—the notion that evolution is a directed, purposeful process—because such thinking has been documented previously (e.g., Bishop & Anderson, 1990; Demastes, Good, & Peebles, 1995, 1996; Kelemen, 1999; Kelemen & DiYanni, 2005; Settlage, 1994). It is also prevalent in society more generally (American Museum of Natural History, 1994; Harris, 2005; Miller, Scott, & Okamota, 2006; National Academy of Sciences, 1998) despite all the evidence to the contrary that supports the contention that evolution is simply adaptation to local circumstances; there is no general pattern of gradual, directed progress.

Our studies provide baseline data that begin to document how college students conceptualize the evolutionary relationships depicted in noncladogenic diagrams and how they think about the underlying evolutionary processes. We make recommendations about the use of particular diagrams in biology education and discuss which aspects of evolutionary theory appear to present the most problems to students in light of particular diagrams.

Study 1

This is a naturalistic study investigating students' interpretations of evolutionary relationships depicted in noncladogenic diagrams typical of those found in textbooks and other sources. Because such diagrams are not standardized in any way, we wrote an evolutionary relationship question that was deemed sensible given the relationships depicted in each diagram.

Method

Subjects. The subjects were 50 students attending a medium-sized, private, Research I university in the southern US who participated in partial fulfillment of course requirements for their zoology class ($n = 11$; 6 females, 5 males) or for extra credit in one of several psychology classes ($n = 33$; 28 females, 5 males) or the ecology class ($n = 6$; 5 females, 1 male). All students had taken biology in high school. Sixteen students had taken no organismal or evolution-related biology courses in college, 14 had taken a single college course (10 a nonmajors class), 8 had taken 2–3 courses (the year-long introductory biology class for biology majors, possibly plus current enrollment in the zoology class), and 12 had taken 4–6 courses (the year-long introductory class for majors plus 2–4 other classes for majors).[1] Thus our sample is representative of students with a wide range of biology background. All of the subjects but one was an undergraduate.

Materials

OVERVIEW. We investigated four noncladogenic diagrams in this study. Two represent "hominid"[2] relationships. Such diagrams abound in the popular press, on many web sites devoted to human evolution, in general biology textbooks at the high school and college levels, and in some scientific journals. These diagrams are of various types and depict relationships in different ways (Catley & Novick, 2008). The context and rationale for a particular diagrammatic format are generally poorly documented. Figure 3, a version of which we have seen in two high school textbooks (Johnson, 1998; Johnson & Raven, 2001), is typical of the numerous diagrams that present the evolution of *H. sapiens* as a linear anagenic event (Catley & Novick, 2008). Such diagrams persist in textbooks despite modern understanding that human evolution followed the same cladogenic principles as that of nonhuman taxa (e.g., Foley, 1987; Johanson & White, 1993; Wood, 1992). Figure 4, the second "hominid" diagram we used, is from a recent issue of *Nature* (Lahr & Foley,
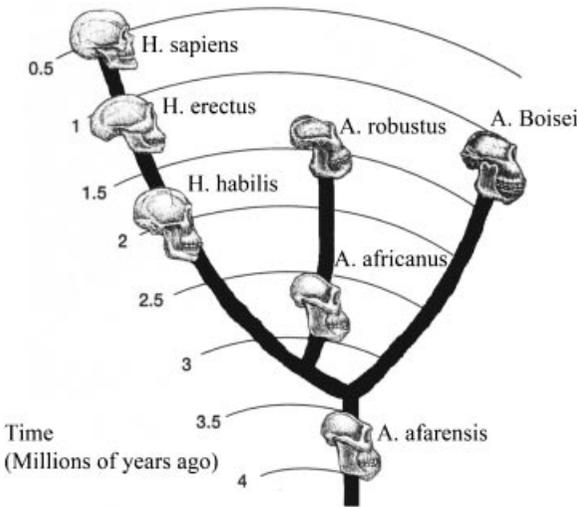
Figure 3. A diagram representing evolutionary relationships among hominoid taxa. (This version, used in Study 1, was adapted from http://www. starsandseas.com; nearly identical versions can be found in Johnson, 1998 and Johnson & Raven, 2001.) This diagram is not a cladogram.

2004). It depicts the putative relationships across time and space between a recently discovered species of *Homo*, *H. floresiensis*, and other species in the genus.

The third diagram is a version of the classic "evolution of the horse" that has been used for generations in school and college biology texts to depict the evolution of *Equus*, the modern horse (see Figure 5). Such diagrams continue to appear in biology textbooks (Catley & Novick, 2008) even though more scientifically accurate cladogenic representations exist (e.g., Evander, 1989; Hulbert, 1989; McFadden, 1992). A version of the diagram used in our study is found in the human biology text (Chiras, 2002) used at the institution where we collected our data.

The fourth diagram is a version of Haeckel's famous tree (see Figure 1). Although nowadays this diagram is used mostly to illustrate evolutionary thinking in the late 1800s and early 1900s, it is still used as an icon of "the tree of life." More importantly, stylized versions of this type of representation are relatively common in modern textbooks. Catley and Novick (2008) examined the evolutionary diagrams found in 27 recent biology textbooks written for high school and college students. Their analysis revealed that modern-day, Haeckel-like diagrams showing a progression from "simpler" to more "complex" taxa as one moves from lower to higher on the diagram or having the topology of an actual tree are found in more than half of these textbooks.
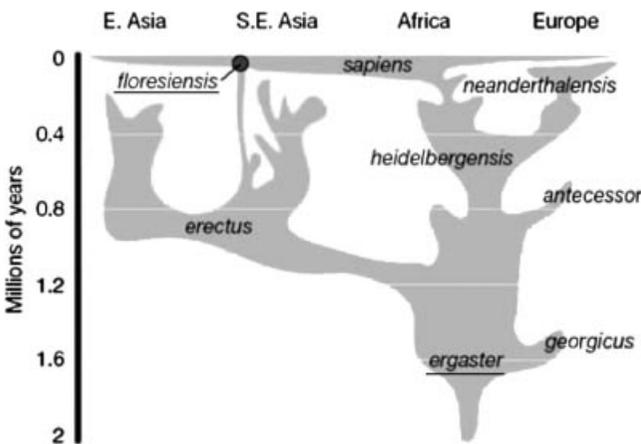

Figure 4. A diagram representing *Homo floresiensis* in the context of the evolution and dispersal of the genus *Homo* (adapted with permission from Lahr & Foley, 2004). This diagram is not a cladogram.
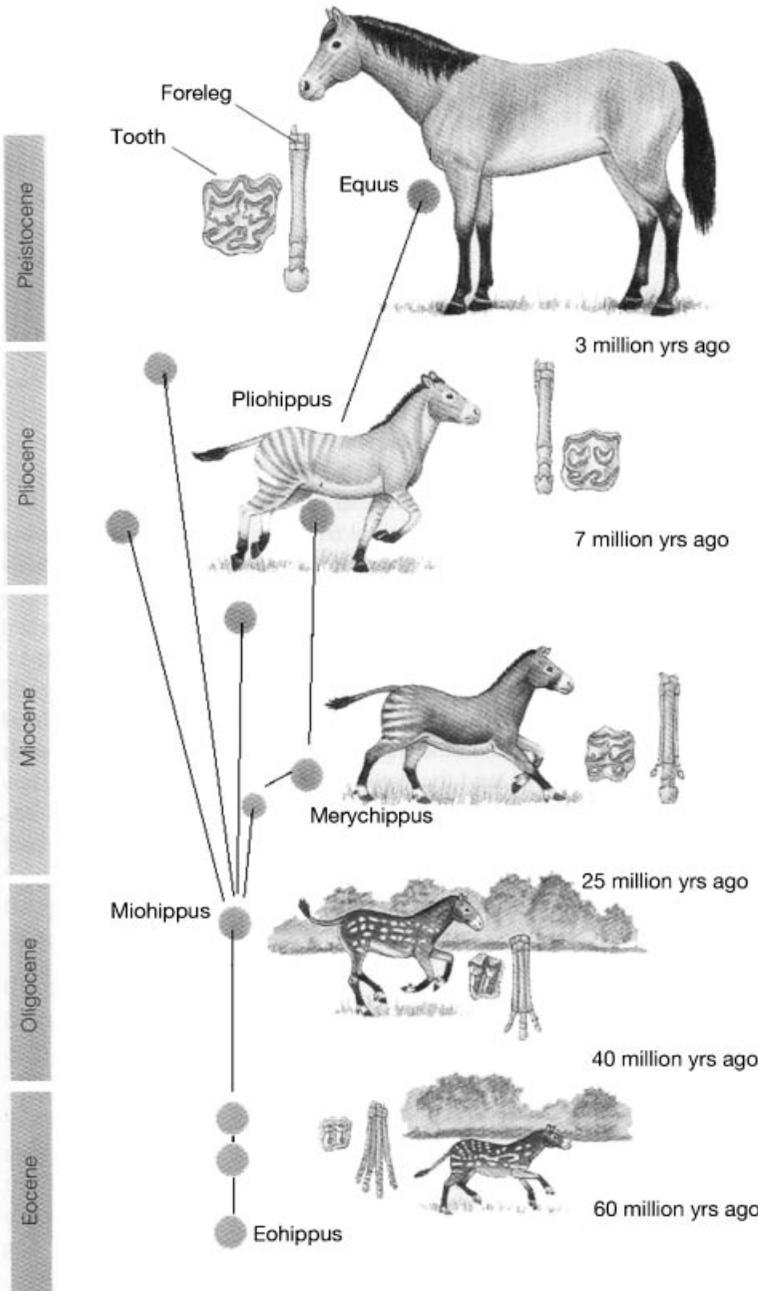
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Figure 5. A diagram representing evolutionary relationships among horse taxa. (This version, used in Study 1, was adapted from http://darwiniana.org/horses.htm#Horses; a nearly identical version can be found in Chiras, 2002.) This diagram is not a cladogram.

The linear *Homo* and horse diagrams are quite similar in structure. The Haeckel and *floresiensis* diagrams, in contrast, are quite different from the other two, as well as from each other. We discuss each diagram in more detail in the following paragraphs.

HOMO DIAGRAM. This is a branching diagram that presents the relationships among four species of *Australopithecus* and three species of *Homo* (Figure 3). The different species are represented by illustrations

of distinctly different skull morphologies. The diagram also contains a time axis (presented in terms of millions of years ago) and has putative ancestors assigned to internal nodes or branches. Subjects were asked: ''In the following diagram, a single branch connects *H. habilis*, *H. erectus*, and *H. sapiens*. What does this single branch tell you about the evolutionary relationship between *H. habilis* and *H. sapiens*?'' Note that in this question, and in the questions asked about each of the other diagrams (described in the following paragraphs), subjects were specifically asked to respond based on what the diagram, or a specified part of the diagram, shows, rather than reporting what (if anything) they happen to know from prior knowledge about the evolutionary relationships among the designated taxa. Although a branching event suggests (incorrectly) that *A. afarensis* is the MRCA of all the other species depicted—both *Homo* and *Australopithecus*, no branching events are depicted among members of the genus *Homo*, which are represented linearly along a single branch. Thus, contrary to the accepted explanation of evolution, based on *this* diagram, the most parsimonious explanation is that one species of *Homo*, over time, turned into, or became, the species that follows it. That is, this diagram depicts anagenesis among the *Homo* taxa.

HORSE DIAGRAM. Like the *Homo* diagram, the horse diagram (Figure 5) shows an unbranched line connecting three taxa—*Merychippus*, *Pliohippus*, and *Equus*. In addition, there are other branches that precede or run concurrently with the branch in question. Thus, for example, the diagram shows that *Miohippus* appeared to give rise to a radiation of at least four taxa, only one of which, *Merychippus*, led to a lineage that resulted in the modern horse *Equus*. Each named horse taxon is represented by a picture of the whole organism together with pertinent character information in the form of images of forelimb and tooth morphology. The diagram has two time axes—geologic epochs on the left and millions of years ago on the right. Subjects were asked: ''In the following diagram, there are branches connecting *Merychippus* to *Pliohippus* and *Pliohippus* to *Equus*. What do these branches tell you about the evolutionary relationships among these taxa?'' Like the *Homo* diagram, this diagram depicts anagenesis among the indicated taxa.

FLORESIENSIS DIAGRAM. This diagram (Figure 4) depicts a variety of information about eight species in the genus *Homo*. Time is indicated in millions of years at the left edge of the diagram. Geographic location is noted at the top. Inside the diagram is an irregularly shaped gray mass whose width varies at different locations. Little ''fingers'' protrude from the gray mass at several points and then abruptly stop. The taxa names are printed in various places on the gray mass or on the protruding fingers. We directed subjects' attention to two taxa—*H. ergaster* and *H. floresiensis*—by underlining their names.

Subjects were asked: ''The following diagram shows a variety of information (e.g., time, location, etc.) about various species of the genus *Homo* (e.g., *H. erectus*, *H. sapiens*, etc.). According to the diagram, what is the evolutionary relationship between *H. ergaster* and *H. floresiensis*?'' The diagram shows that *H. ergaster* is located in an earlier time period than *H. erectus*, to which it is connected by a thin ''bridge'' of gray. *H. erectus* in turn is connected to *H. floresiensis* by an even thinner thread of gray. Although these species are not laid out in a strictly linear fashion, the depiction clearly shows connections across time and space. Would students interpret *H. ergaster* as the MRCA of *H. sapiens* and *H. erectus*, or would they interpret the diagram as depicting anagenesis from *ergaster* to *erectus* to *floresiensis*?

HAECKEL'S TREE. Haeckel's famous ''evolutionary'' diagram (Figure 1) depicts the array of life as a spreading, branching tree. Taxa are ranked from the base (Monera) up to the crown (''Man''), with some appearing on the trunk (e.g., marsupials) and others on branches (e.g., rodents). Four taxa—Protozoa, Invertebrate Metazoa, vertebrates, and mammals—are found along the right side of the tree, again ranked from the base (Protozoa) to crown (mammals). Although time is not depicted directly on this diagram, it is implicit in the tree representation—everyone knows that higher branches on a tree reflect later growth. Subjects' attention was drawn to two taxa—marsupials and rodents—by adding arrows to the diagram indicating these taxa. Subjects were asked; ''In this diagram, some taxa are on the main trunk and some taxa are on the branches. Consider, for example, marsupials and rodents. According to the diagram, what is the evolutionary relationship between these two taxa?''

This diagram is the epitome of a directed, teleological view of evolution. As can be seen in Figure 1, successive taxa are arranged so as to represent an increase in ''complexity'' from those that precede it.

"Man," being at the top of the tree, is obviously the most complex species and represents the pinnacle of evolution, despite the fact that, arguably, snakes are the most highly evolved vertebrate (Shine, 1998). In Haeckel's tree, in contrast, snakes are located far below *H. sapiens*, at the very tip of the most strongly downward-leaning branch on the entire tree.

At the same time, this diagram provides a wealth of potentially informative branching events, putative MRCAs, extinction events, and even clades that are the result of radiations of taxa. Subjects have the opportunity to refer to a branching event in answering the question about the evolutionary relationship between marsupials and rodents. According to the diagram, there is a putative MRCA shared by ((rodents) + (Sirena + ungulates)). It is ambiguous whether this MRCA evolved subsequent to marsupials or whether marsupials are in fact the MRCA of this clade. We were interested to see whether, despite the teleological depiction of evolution, this diagram might lead some students to express a more appropriate cladogenic understanding.

Design and Procedure. The four diagrams were divided into two pairs, which were distributed to different subjects. One member of each pair depicted "hominid" taxa and the other did not: (a) *Homo* and Haeckel ($n = 23$) and (b) horse and *floresiensis* ($n = 27$). Each pair was appended to a problem booklet involving data collection for several separate studies addressing distinct conceptual and theoretical issues.[3] The results from other parts of the booklet are reported elsewhere (Novick & Catley, 2007).

Subjects participated individually or in small groups in a single session that took place outside of class in a laboratory room or classroom on campus. Each subject completed the booklet on his/her own without the use of any outside resources. Subjects worked through the problem booklet at their own pace, taking about 45–60 minutes to complete it.

Results

The results are organized into three broad sections. First, we describe how we coded the data and report the reliability of our coding scheme. Next, we present the results of preliminary analysis to justify collapsing the data across the *Homo* and horse diagrams. Finally, we present subjects' responses to our questions about the four diagrams.

Coding the Data. We coded subjects' responses on a number of variables, described in this section, that were grouped into four broad conceptual categories: evolutionary relations, evolutionary processes, time, and other. The specific codes were the same for all four diagrams (except that there were two idiosyncratic codes for the *floresiensis* diagram). Examples of subjects' responses that fit the various coding categories are given in conjunction with the results.

EVOLUTIONARY RELATIONS. We coded each subject's response for the presence or absence of each of six types of terms indicating the nature of the evolutionary relation depicted. These six codes were then combined into three categories for analysis, with each category being coded as 0 (the requisite term was absent from the subject's response) or 1 (the requisite term was present in the subject's response). The first category—evolve into/from—combined three separate codes: (a) evolved into, speciated into, speciated to/from, evolved to be, became; (b) evolved from, speciated from, derived from, developed from, came from, evolved out of; and (c) evolved through or transition stage. This category of responses would seem to reflect a primarily anagenic understanding of evolution. According to Lakoff and Johnson (1980), in their book on the metaphorical nature of language, the use of *into* or *out of* in an expression—for example, "I made a sheet of newspaper *into* an airplane" (p. 73), "the caterpillar turned *into* a butterfly" (p. 74), "mammals developed *out of* reptiles" (p. 74)—reflects a change of kind; what was once one kind of thing is now a different kind of thing.

The second category—ancestor/descendant—combined two separate codes: (a) ancestor of, ancestor to, line of ancestry and (b) descended from, descendant of. The third category involved a single code, indicating whether the subject talked about a common ancestor for any of the taxa in the diagram. These latter two categories may reflect a somewhat more sophisticated understanding of evolutionary relationships.

CHARACTERS AND EVOLUTIONARY PROCESSES. We also coded each written response with respect to whether the subject mentioned (a) characters possessed by one or more taxa depicted on the diagram and (b) any of a

variety of evolutionary mechanisms. Answers that received these codes likely reflect a more than superficial familiarity with evolutionary processes. There were two character codes, indicating whether the subject wrote about characters generically (e.g., using words such as *characteristics* or *traits*) or specifically (e.g., mentioning tooth structure for the horse diagram). There were eight evolutionary process codes, each of which indicated whether the subject mentioned a particular process-related aspect of evolution: (a) any reference to change; (b) speciation, creation of new species; (c) splitting, branching, diverging; (d) adaptation, advantage, fitness; (e) mutation; (f) extinction; (g) reproductive isolation; and (h) role of the environment. Because the last four of these codes occurred very infrequently, they were collapsed to create a general category (coded 0 or 1) of other evolutionary processes.

TIME.   We also coded each response for whether the subject mentioned time. One code was used when subjects referred to time generically, using words such as *over time*, *in order*, and *earlier*. A second code was used for specific references to time, such as a certain number of million years ago or during a particular geologic epoch.

OTHER CODES.   Finally, there were three additional codes that do not fit into any of the previous categories. For all four diagrams, we coded whether subjects used arrows in their response (e.g., *erectus → ergaster*). In addition, for the *floresiensis* diagram, we coded whether the subjects mentioned (a) where taxa were located (e.g., S.E. Asia) or (b) migration. No subject mentioned these topics for any other diagram, presumably because only the *floresiensis* diagram specifies regions of the world.

INTER-RATER RELIABILITY.   The three authors independently coded all the responses. Inter-rater reliability was computed as the number of agreements divided by the total number of codes given (agreements plus disagreements). We counted as an agreement any time at least two of the three coders said a particular code applied. If only one coder said a code applied, this was counted as a disagreement. (Disagreements were resolved by discussion.) Inter-rater reliability was computed based on the separate codes that were given, before codes were combined for analysis. The agreement rates were 89% for the *Homo* diagram, 85% for horse, 100% for Haeckel's tree, and 88% for *floresiensis*. Collapsing across diagrams, the overall agreement rate was 89%.

Preliminary Analyses.   As noted earlier, the *Homo* and horse diagrams are structurally very similar. Moreover, we asked a similarly worded question about isomorphic portions of the two diagrams. In particular, we asked about the evolutionary relationship among three taxa arranged along a single line. It seems reasonable to expect, therefore, that subjects' responses would be similar for these two diagrams. To address this issue, we conducted a *t*-test comparing the *Homo* and horse diagrams for each coding category. None of the results reached the conventional level of statistical significance ($p < 0.05$). Because students responded similarly to these two structurally similar diagrams, we report the results collapsed across these two diagrams. This facilitates comparing students' responses to this type of diagram to their responses to the other two diagrams—Haeckel's tree and *floresiensis*—which are quite different. In particular, this helps clarify the extent to which the different types of diagrams yield similar or different interpretations of evolutionary relationships.

Evolutionary Relations Codes.   The primary goal of this naturalistic study was to determine what kind of understanding of evolutionary relationship is prompted by noncladogenic diagrams among college students. As such, our data are largely descriptive. The bar graph in Figure 6 shows the proportion of subjects who received each code. As noted earlier, the data for the *Homo* and horse diagrams are collapsed.

EVOLVE INTO/FROM.   Subjects were most likely to give evolve into/from answers for all four diagrams, with an average of almost 60% of subjects making reference to one species evolving into or from another species (Figure 6). This is at least twice as many subjects as gave the ancestor/descendant or common ancestor responses. Despite the differences among the diagrams, most students explained all four sets of evolutionary relationships in a manner strongly suggesting that they interpreted the depictions as one entity becoming another, a hypothesis we tested in Study 2. A more sophisticated response would involve the
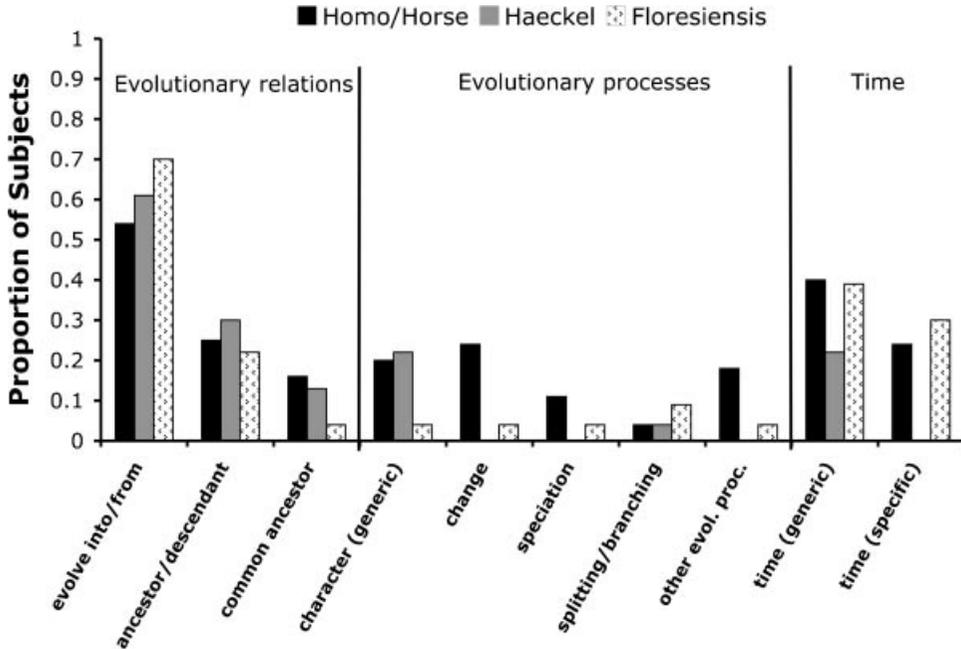
Figure 6. Subjects' responses to the evolutionary relations questions for each diagram in Study 1.

concept that one taxon shares a MRCA with another rather than evolving "from it." As shown in Figure 6, mention of common ancestry was very rare.

The following statements are examples of the kinds of responses that received the evolve into/from category code. (a) *Homo*: "There was a evolutionary transition stage *H. erectus*." (b) horse: "That the eohippus change over time to become the equus." (c) Haeckel: "Rodents evolved from marsupials." (d) *Floresiensis*: "*H. floresiensis* evolved from *H. ergaster* over a period of 1.6 million years. *H. ergaster* evolved into *H. erectus* over 0.8 million years, and then to *H. floresiensis* over another 0.8 million years."

DISCUSSION OF ANCESTRY. Averaged across the four diagrams, 25% of subjects used the term *ancestor* or *descendant* (or both). For example, one subject wrote that the Haeckel diagram shows that "rodents descended from marsupials." For the *Homo* diagram, another subject wrote that "*Homo habilis* is an ancestor of homo sapien [sic]." We hypothesize that use of the concepts of ancestor and/or descendent reflect a somewhat more sophisticated understanding of evolutionary processes than is apparent in the use of evolve into/from. Ancestor and/or descendent suggest a grasp of the notion that any given taxon arose, not as a result of some other taxon becoming it, but due to an ancestral population split that gave rise to two separate taxa. Note, however, that subjects sometimes used both types of terms in the same response. For example, one subject wrote the following about the *floresiensis* diagram: "According to the diagram, floresiensis evolved from ergaster. Over a time span of millions of years, ergaster evolved into erectus & moved from Africa to S.E. Asia. Then, erectus evolved into floresiensis. Ergaster is an ancestor of floresiensis."

Use of the term *common ancestor*, arguably an even more sophisticated concept, was rare, being invoked by an average of only 12% of subjects. One subject wrote that the *Homo* diagram "tells us that all three *H. habilis*, *H. erectus*, and *H. sapiens* evolved in that order (chronologically) from common ancestor *A. afarensis*." Another subject wrote that Haeckel's tree shows that "rodents along with cogulates [sic] and sirena evolved from marsupials. The marsupial is the common recent ancestor to sirena & rodents." For the horse diagram, one subject wrote, in part: "All these taxa share a common ancestor. The closest common ancestor is merychippus and fr/that stage the taxa has evolved. The species has evolved over the las [sic] 10 million yrs to become equus . . ."

Evolutionary Processes Codes. It is important to note that subjects were not specifically asked to provide process-based answers to our questions. Nevertheless, some subjects included elements of evolutionary processes in their answers. As shown in Figure 6, individual evolutionary process codes were given for the responses of up to 24% of subjects, depending on the diagram. In contrast to the evolutionary relations codes, references to evolutionary processes varied more across the diagrams. That is, subjects were more likely to mention the processes they believed to have led to the depicted evolutionary relations for some diagrams than for others.

CHARACTERS. The characters code was included under evolutionary processes because conceiving of taxa in terms of attributes that are subject to selection by the environment is a prerequisite for considering adaptation, a very important evolutionary process. An average of 17% of subjects made generic references to characters (although such references were less common for *floresiensis* than for the other three diagrams). For example, for the horse diagram, one subject wrote: ''It implies that they have direct connections and characteristics over nearly 23 million year ago. It also shows that the evolution of the animal has not extraordinarily changed, but does display some similar characteristics.'' For Haeckel's tree, one subject wrote: ''Marsupials are an ancestor of rodents & they should share many common features; rodents evolved later than marsupials (probably have some characteristic marsupials don't). Only separated by one branch & one level so fairly closely related.''

We also coded whether subjects mentioned specific characters (i.e., specific morphological features of the taxa depicted), but it turned out that such responses were given only for the horse diagram (33% of these subjects), in which pictures of forelimbs and teeth were prominently displayed alongside the pictures of the horses: e.g., ''Over time, their foot anatomy & tooth structure have evolved w/the changing environmental conditions in which they dwell. Now on flat land, the Equus has herbivorous flat teeth & flat hooves. Long ago when the structure of the land was different & plant availability was also, Eohippus had to have toes & sharper teeth.''

EVOLUTIONARY CHANGE. Reference to change was almost exclusively found in the *Homo* and horse diagrams (average of 24% of subjects), perhaps because those two diagrams seem to clearly show one taxon changing into another. Most subjects mentioned that either a particular character or a particular taxon changed. For example, one subject wrote about the *Homo* diagram that ''it tells us that *H. sapiens* evolved over time, through *H. erectus*, with changes to different structures within the body from *H. habilis*.'' Another subject wrote that the horse diagram indicates that ''the equus is descendant of pliohippus and pliohippus is a descendant of merychippus. Merychippus evolved over time and these evolutionary changes led to the creation of two new species.''

Change is a very colloquial concept that may differ greatly across domains. In evolutionary biology, the type of change that is meaningful is adaptation driven by environmental conditions. Accordingly, we coded subjects' references to adaptation. The results are not included in Figure 6 because this code was essentially only given for the horse diagram (22% of subjects; one subject—4%—also received this code for the *Homo* diagram). For example, one subject wrote that ''the horse was a small animal with short legs. It did not have that much hair. The horse adapted to the changes in the environment and has stronger bones and is a bigger animal.'' Another subject was less eloquent: ''These branches tell that one species (such as the pliohippus) adapted and evolved into another species (such as the equus).'' While reference to the concept of adaptation for the horse diagram is encouraging, it should be pointed out that adaptive characters (pictures of teeth and forelimbs) were prominently displayed on the diagram. Perhaps more instructive is the fact that this term or way of thinking was (essentially) absent in subjects' responses to the other three diagrams, even though distinctive pictures of skulls are provided in the *Homo* diagram.

THE FORMATION OF SPECIES. Speciation—the process of formation of a new species—is an extremely important evolutionary concept. It was referred to by 11% of subjects overall, mostly for the *Homo* and horse diagrams. Most (80%) of the subjects who mentioned speciation also mentioned change, suggesting perhaps that change is a mechanism that can result in speciation. For example, for the horse diagram, one subject wrote: ''All these taxa share a common ancestor. The closest common ancestor is merychippus and fr/that

stage the taxa has evolved. The species has evolved over the las [sic] 10 million yrs to become equus. They all share similar traits (tooth & foreleg) but the formation of species is due to change over time.''

The scientifically accepted mechanism for speciation is a branching or splitting event, as discussed in the Introduction Section. References to splitting, branching, or diverging were rare in our data set (an average of only 5% of subjects). One subject wrote the following about the *floresiensis* diagram: ''*H. floresiensis* was initially *H. ergaster*. From the *H. ergaster* two major branches of Homos formed. From *H. ergaster H. erectus* evolved & split into 2 categories. From one, the *H. floresiensis* evolved.'' Another subject mentioned the idea of splitting in response to Haeckel's tree: ''They are both mammals that evolved from the theomorpha vertebrates. Rodents descended from marsupials, and have thus evolved more over time to vary from them. The vast amount of the trunk that supports these two taxa jointly indicates that they descend from a long common evolution over time until they finally split and evolved separately among many other species at the top of the tree.''

OTHER EVOLUTIONARY PROCESSES. This category included mutation, extinction, reproductive isolation, and the role of the environment. Because none of these concepts were mentioned often enough to be considered on its own, we combined these four codes into a general ''other evolutionary processes'' code for the purpose of analysis. Although other concepts are equally, if not more important in understanding how evolution works (e.g., variation within species), these were the specific additional concepts that were (occasionally) mentioned by our subjects. Because our subjects were asked about specific evolutionary relationships, not the processes that generated them, we cannot draw conclusions about students' knowledge, or lack thereof, of any concepts they failed to mention (Ericsson & Simon, 1980).

On average, 10% of subjects mentioned a process in this category. Almost all of these responses were for the *Homo* and horse diagrams, perhaps because the depiction of one taxon apparently changing into another seems to call for a process explanation. We tested this hypothesis in Study 2. The following response for the *Homo* diagram mentioned mutation: ''The branch tells us that they both descended from *A. afarensis*, but that *H. sapiens* came after *H. habilis*. Over time, *H. habilis* evolved into *H. sapiens* after mutations changed them and the ones most fit to survive did.'' For the horse diagram, the following response mentioned reproductive isolation: ''These branches indicate that the species Merychippus was an ancestor of Pliohippus and Pliohippus that of Equus (as characteristics of these ancestor species changed, populations became reproductively isolated, forming new species).'' Another response for the horse diagram mentioned the role of the environment: ''That this how the modern day horse evolved from a species over millions of years. It shows exactly when the animal adapted/changed/evolved to become better suited w/ its environment & what changes took place.''

Time Codes. References to time were coded as either generic or specific. Generic references figured prominently across the four diagrams, averaging 35% of subjects. For example, one subject wrote that Haeckel's tree shows that ''rodents evolved from a common ancestor with marsupials; they share the traits of marsupials but also evolved many differences over time.'' Specific references to time were confined to the *Homo*, horse, and *floresiensis* diagrams. There were fewer specific than generic references to time—an average of 25% of subjects across these three diagrams. One subject made such a (incorrect) time reference for the *Homo* diagram: ''That 2 billion years ago *H. sapiens* did not exist. Their ancestor (*H. habilis*), however, did.'' Generic time references occurred less often for the Haeckel diagram than for the other three diagrams (means of 24% and 40%, respectively). These differences across diagrams are not surprising given that time axes, in terms of either geologic epochs or millions of years, are a prominent feature of the *Homo*, horse, and *floresiensis* diagrams. The Haeckel diagram, in contrast, does not include an explicit time axis.

Other codes. An idiosyncratic answer confined to 15% of subjects for the floresiensis diagram and one subject (4%) for the horse diagram involved using arrows to connect the taxa in question. For example, for the floresiensis diagram, one subject simply wrote ''floresiensis → erectus → ergaster.'' Other subjects wrote something in addition to the taxa connected by arrows. Although the arrows presumably indicate an ordering of the taxa (Tversky, Zacks, Lee, & Heiser, 2000), the dimension on which the taxa are ordered (time or something else) is unclear. Moreover, it is unclear whether the arrows are intended to convey meaning beyond sequential ordering (e.g., transformation, ancestry).

In respect to location and migration in relation to the *floresiensis* diagram, substantial numbers of subjects mentioned the gray areas as potentially indicating location in space or movement. Some 43% of subjects mentioned location, and 22% indicated the diagram represented migration of various *Homo* species. For example, one subject wrote ''That as the ergaster moved to different areas of the world there evolved diff. species, i.e. the floresiensis evolved from the ergaster when they started to S.E. Asia.''; another wrote that ''Ergaster migrated to diff areas, such as Asia & became erectus, which then moved into 2 separate grps (E. & S.E. Asia) & those in S.E. Asia became Floresiensis.''

Discussion

We asked university students to tell us what four diagrams (Figures 1, 3–5) indicate about the evolutionary relationships among specific taxa depicted in those diagrams. Although students' responses to questions posed to them always reflect a combination of the information they are given to evaluate and their pre-existing content knowledge, we took great care in wording our questions to make it clear that we wanted to know what the diagrams show about the evolutionary relationships among certain taxa. Our analysis of these responses suggests persistent patterns in students' understanding of evolution that indicate they view the evolution of the taxa in these diagrams to reflect an anagenic rather than a cladogenic process.

As shown in Figure 6, most of our subjects interpreted the four diagrams to depict one taxon evolving into or from another (average of almost 60% across diagrams), an interpretation that suggests anagenic rather than cladogenic processes (see Lakoff & Johnson, 1980). Such an interpretation is also strongly supported by the students' quotations in the results section. That is, they understood the diagrams to show that evolution involves one taxon (e.g., *H. erectus*) changing into another taxon (e.g., *H. sapiens*) over time. In this model of species genesis, one assumes that the original species becomes extinct during this process. Our subjects rarely mentioned these extinctions. Modern evolutionary thinking, in contrast, understands that evolution involves cladogenesis, a process whereby one species splits into two. Even though Haeckel's tree (Figure 1) and the floresiensis diagram (Figure 4) potentially show branching at the points subjects were asked to consider, anagenic responses were consistently high across all diagrams.

The results of this study provide an intriguing window into students' interpretations of these particular evolutionary diagrams. However, we cannot know precisely what students mean when they say that one taxon evolved into or from another taxon or was the ancestor or descendant of another taxon. Study 2 was designed to address this limitation. In particular, we presented these terms in an evolutionary context and asked students what they mean. Given the results of Study 1, we made two predictions concerning the results of Study 2. First, we predicted that students would be more likely to refer to one taxon turning into another taxon (i.e., anagenesis) when given the evolved into/from terms than when given the ancestor/descendant terms. Second, recall that in Study 1 most of the evolutionary process responses were for the *Homo* and horse diagrams, which depict one taxon changing into another. We argued that such a depiction seems to call for an explanation of how that transformation might have happened. Accordingly, we predicted that if evolved into/ from suggests anagenesis, students who received those terms would mention more evolutionary processes than would students who received the ancestor/descendant terms.

Study 2

To investigate subjects' interpretations of the specific evolutionary terms found in the Study 1 results, we presented these terms in the context of the evolutionary relationship between the jumping ground bug and the assassin bug. The choice of these taxa was made after careful consideration. By choosing taxa that were essentially unknown to our subjects, and about which the actual evolutionary relationship was unknown, we hoped to get clear explanations of what the terms mean without subjects' answers being mediated by prior knowledge or alternative conceptions.

Method

Subjects. The subjects were 62 students who were recruited from the same university as the subjects in Study 1. They participated in partial fulfillment of course requirements for introductory psychology (7 females, 3 males) or for extra credit in the psychology (8 females, 1 male, 1 unknown sex), education

(22 females, 4 males), or biology (11 females, 4 males, 1 unknown sex) class from which they were recruited. This sampling method provides a diverse cross-section of the undergraduate population at the university in question.

Design and Materials. Subjects were randomly assigned to explain one of four evolutionary terms. In all conditions, subjects received the following scenario: ''Another student tells you about the evolutionary relationship between the now extinct jumping ground bug and the assassin bug.'' The nature of the evolutionary relationship between the two bugs was then described using one of four terms, based on the results of Study 1. These terms were evolved into ($n = 14$), evolved from ($n = 16$), is an ancestor of ($n = 16$), and is descended from ($n = 16$). For example, in the evolved-into condition, the scenario continued as follows: ''This student tells you that **the jumping ground bug <u>evolved into</u> the assassin bug**. Explain what the term ''**evolved into**'' means so that a 9th grader would understand it.'' In the descended-from condition, in contrast, the second sentence of the scenario was as follows: ''This student tells you that **the assassin bug is descended from the jumping ground bug**.'' We expected that asking subjects to provide an explanation that a ninth grader would understand would elicit clear descriptions of how they interpreted the indicated evolutionary term (e.g., see Novick, 2004; Novick & Hurley, 2001).

Procedure. The question for this study was included in a questionnaire that appeared as the final part of a multi-part booklet that involved data collection for several separate studies. These studies addressed issues concerning students' understanding of cladograms (Morabito, Catley, & Novick, 2010; Novick & Catley, 2007, 2010) and evolutionary deep time (Catley & Novick, 2009).[4] Subjects participated individually or in groups in a laboratory room or classroom on campus. Each subject completed the booklet on his/her own without the use of any outside resources. Subjects worked through the booklet at their own pace, taking approximately 45–70 minutes to complete it.

Results and Discussion

Coding the Data. Subjects' responses were mostly coded as described for Study 1. In particular, we gave the same evolutionary relations, evolutionary processes, and time codes. We also gave two new codes, not used in Study 1, that are described later in this section.

As in Study 1 the evolutionary relations codes were grouped into three categories for analysis: evolve into/from, ancestor/descendant, and common ancestor. The evolutionary process codes were grouped into seven categories for analysis: (a) generic character; (b) any mention of change; (c) adaptation or selection; (d) speciation, creation of a new species; (e) splitting, branching, diverging; (f) role of the environment; and (g) other evolutionary processes. This coding scheme reflects several small changes from Study 1. First, subjects in this study never referred to specific characters, presumably because we did not tell them about any such characters for the bugs in question. Thus, that code was dropped. Second, the environment code was kept separate rather than being included in the other-evolutionary-processes code because it was one of the more frequently given process codes. Thus, the other-evolutionary-processes code included only mutation, extinction, and reproductive isolation. The generic time code was the same as in Study 1. No subjects referred to specific time periods, presumably because no time scale was included in the study materials. Therefore, that code was dropped.

The two new codes were anagenesis and purpose. We gave the anagenesis code when a subject's response conveyed the idea of anagenesis, that is, that one bug (e.g., the jumping ground bug) turned into or became the other bug (the assassin bug) over time. We gave the purpose code when a subject's response described evolution as a purposeful (teleological) process. For example, we gave this code when subjects wrote that the jumping ground bug had to develop new traits in order for the species to survive (often becoming the assassin bug in the process, thereby also earning the anagenesis code). Both of these new codes reflected a qualitative assessment of what the subject wrote rather than an indication of specific words used, as did the other codes.

Subjects' responses were coded independently by the second and third authors, who were blind to which evolutionary term subjects received. Inter-rater reliability was computed as the number of agreements divided by the total number of codes given (agreements plus disagreements). As in Study 1, inter-rater

reliability was computed based on the separate codes that were given, before codes were combined for analysis. Overall agreement for all of the codes was 92%. Discrepancies were resolved through discussion.

Analyses of the Individual Codes.

OVERVIEW. Conceptually, evolved into and evolved from are comparable, differing only in the direction of comparison of the two taxa. The same is true for ancestor of and descendant of. It makes sense, therefore, that we saw a similar pattern of results across codes for the evolved-into and evolved-from conditions and for the ancestor-of and descendant-of conditions. Thus, we combined the two terms in each conceptual pair for analysis. Figure 7 shows the proportion of subjects in the evolved into/from and ancestor/descendant of conditions who received each code.

We conducted a one-factor between-subjects analysis of variance (ANOVA) on each code that was received by at least 20% of the subjects (see Table 1). As shown in Figure 7, this criterion excludes three codes that were given to the responses of no more than 8% of the subjects: Ancestor/descendant, common ancestor, and splitting/branching.

EVOLUTION AS PURPOSE-DRIVEN ANAGENESIS. Change, environment, purpose, and anagenesis all showed a significant main effect of the evolutionary term used (see Figure 7). These results suggest that the terms evolved into and evolved from imply an alternative conception of the process of evolution, one in which organisms and not taxa change so that they can better cope with a new environment, and in accomplishing this goal they become a new species. One of biggest obstacles educators need to overcome in evolution education is the teleological mindset that evolution is a purposeful and directed process.

In Study 1, we found that approximately 60% of students talked about one taxon evolving into or from another taxon, language that we interpreted as suggesting a conception of evolution as anagenesis. In this study, 43% of students who were asked to explain the meaning of evolved into/from gave an answer that indicated anagenesis.
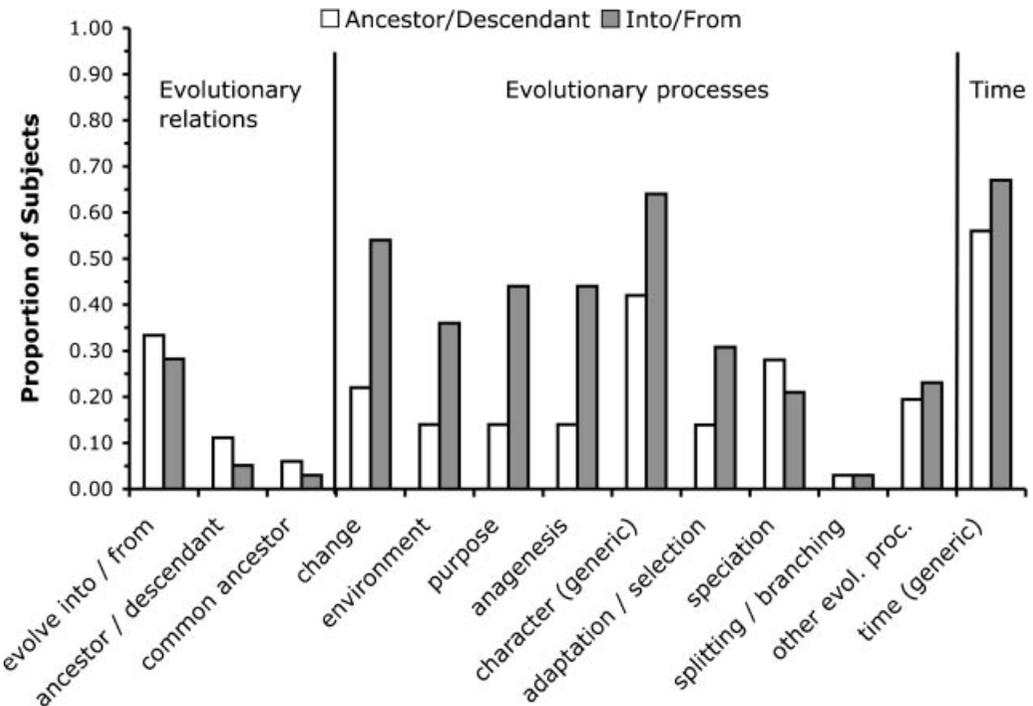

Figure 7. Subjects' interpretations of the evolutionary relations terms used in the bug evolution question in Study 2.

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Table 1
Results of the ANOVAs for the 10 codes that were given to at least 20% of the subjects in Study 2

Code	$F_{(1, 60)}$	p	MSE
Evolved into/from	1.60	> 0.20	0.20
Change	***15.59***	***<0.001***	***0.20***
Environment	***7.66***	***<0.01***	***0.19***
Purpose	***11.31***	***<0.01***	***0.19***
Anagenesis	***6.16***	***<0.05***	***0.19***
Character (generic)	1.69	> 0.15	0.25
Adaptation/selection	2.68	> 0.10	0.18
Speciation	1.79	> 0.15	0.18
Other evolutionary processes	0.03	> 0.85	0.17
Time (generic)	1.24	> 0.27	0.24

Note. Statistically significant effects are highlighted in bold italic type.

More generally, of the 30 students in the evolved into/from condition, 67% ($n = 20$) received at least two of the four component codes (change, environment, purpose, anagenesis) suggestive of the alternative conception. Six subjects (20%) received all four codes, and six subjects received three codes. For example, one subject wrote: ''Evolved into in this case would mean that slowly over time the bug adapted some of it qualities to the changing environment. Thus it soon became so different from the jumping bug it was renamed the assassin bug.'' Similarly, another subject wrote: ''It changed the way that it adapted to its surroundings to survive. The old species doesn't exist anymore because its characteristics changed—it did not just spawn off a new breed. Therefore the old bug ceases to exist!'' A third subject wrote: ''The jumping ground bug existed first and over time adapted to its surroundings and changed. It then grew into or changed into a new entity which is now called the assassin bug.'' Even subjects who received only two of the four codes often gave similar responses. For example, one subject wrote: ''One jumping bug transformed through mutation (changed), and became the assassin bug, over a very long time.'' Another subject wrote: ''the jumping ground bug, over many generations mutated and changed slightly until it had the characterisitcs [sic] that came to be known as indicating an assassin bug.''

EVOLUTION AS A CHARACTER-DRIVEN PROCESS. Across both evolutionary term conditions, 55% of subjects received the generic character code. Thus, approximately half of our subjects may have some understanding that evolution is a character-driven process, regardless of what other alternative conceptions they may harbor. For example, one subject wrote: ''evolved into means that it added new characteristics to its physical attributes (internal, external, or cellualar [sic]) that the original species did not have.''

EVOLUTION AS ADAPTATION/SELECTION. In contrast to the possible appreciation for the role of characters in evolution, only 24% of subjects (collapsed across conditions) received the adaptation/selection code. Moreover, as discussed in the anagenesis section, many of these subjects conceived of this adaptation as purpose-driven rather than environmentally driven. For example, one subject wrote that ''the jumping ground bug had changes in gene frequency (how certain characteristics develop) to help the species better exploit their environment (italics added). As a group, ground bugs slowly became adapted in a new way and 'turned into' assassin bugs.'' Another subject wrote that ''in order to adapt (italics added) to survive in changing conditions, some jumping ground bugs slowly developed traits and eventually evolved into the assassin bug. Those that lacked mutations died off, which is why the jumping ground bug is extinct.''

Number of Process Codes. Recall that we predicted that subjects who received the evolved into/from terms would mention more evolutionary processes than subjects who received the ancestor/descendant terms because the notion of one taxon becoming another seemingly cries out for an explanation of how that could have happened. To test this hypothesis, we computed for each subject the number of different evolutionary processes mentioned. The following codes were included: generic character, change, environment, adaptation/selection, speciation, splitting/branching, mutation, extinction, and reproductive isolation. As

predicted, subjects in the into/from condition mentioned significantly more evolutionary processes than did subjects in the ancestor/descendant condition (Ms of 2.47 and 1.63, respectively), $F(1, 60) = 7.40, p < 0.01$, $MSE = 1.48$.

It is important to acknowledge a limitation of this study, namely its reliance on written responses. Previous research has documented the benefits of interview methodologies for understanding students' conceptions of evolution (e.g., see Treagust & Duit, 2008). Given our large sample, it was not possible to follow-up our written question with an interview. To mitigate this weakness, we asked students to describe what the indicated evolutionary term means so that it would be understandable to a ninth grader.

General Discussion

The scientifically accepted process of speciation is cladogenesis, which involves the splitting of one population into two that are then subjected to different selection pressures due to the different environments in which they reside. In contrast, anagenesis is the process of one taxon turning into a different taxon over time. Catley and Novick (2008) found that many diagrams in biology textbooks are not conceived in a cladogenic framework. That is, these diagrams do not convey patterns of nested sets of taxa supported by MRCAs or are ambiguous as to whether speciation events were the result of anagenesis or cladogenesis. No research to date has examined students' interpretations of evolutionary relationships depicted in noncladogenic diagrams. Catley and Novick (2008) argued that such scientifically inaccurate diagrams may be less effective for instruction and may contribute to misunderstandings of macroevolutionary theory. The two studies reported here tested and found support for the latter contention.

Students' Interpretations of Noncladogenic Evolutionary Diagrams

College students' interpretations of the evolutionary relationships depicted in the noncladogenic diagrams in Study 1 and their explanations of the evolved into/from terminology in Study 2 revealed an anagenic and teleological (purpose-driven) conception of evolution in which (a) *organisms* change so that they can better cope with a new environment and (b) as a result they turn into a new species. Clearly, educators at all levels need to be cognizant of which types of diagrams appear to depict anagenesis and must be vigilant when presenting evolution to ensure that a teleological perspective is absent from instruction. It may help in this regard for educators to stress that it is taxa, not individual organisms that adapt and evolve. An organism is an individual, whereas a taxon is a phylogenetically related set of individuals. If students equate organisms with adaptation, it follows that beliefs about adaptation being a needs-based process driven by an organism's requirements likely will result.

Another important consideration concerns students' lack of understanding of ancestry. In Study 1, only 37% of subjects used terms related to ancestry to describe evolutionary relationships (e.g., ancestor, descendant, common ancestry), compared with nearly 60% who used terms related to anagenesis (e.g., evolved into, became). In Study 2, students were less likely to provide causal explanations for the evolutionary relationship we described when the scenario was presented as an ancestor/descendant situation. They mentioned a mean of only 1.63 of the 9 evolutionary processes we coded, compared with a mean of 2.47 for those in the evolved into/from condition. Clearly, though, causal explanations were infrequent in both conditions. The critical evolutionary mechanism underlying cladogenesis is the notion of branching or splitting. Only 3% of subjects (in both conditions) made any mention of this explanatory mechanism of how one bug may be related to another. These data suggest that neither high school nor college classes are teaching students about critical macroevolutionary mechanisms as part of their regular biology instruction.

The Importance of Character-Based Thinking

Introducing tree thinking into the classroom is considered an important goal of science education by many authors (e.g., Baum et al., 2005; Catley, 2006; Catley et al., 2005; O'Hara, 1988). Two interrelated prerequisites for tree thinking are understanding the importance of variation within species and seeing groups of taxa as supported by derived (evolved) characters. In Study 1, where there was no need for students to talk about processes to answer our evolutionary relationship questions, only about 17% mentioned characters in their responses (mean across the four diagrams). It is important to note, however, that the inclusion of graphics

of characters that define particular taxa in the horse diagram seemed to focus students' attention on the importance of characters. For that diagram, 44% of students made reference either to specific characters (e.g., teeth) or to characters in general. These results suggest that diagrammatic representations of phylogenies should include depictions of important defining characters. Presumably, these depictions could be either drawings (e.g., of hooves with one or three toes) or comparable verbal labels, although we are not aware of any research addressing this issue.

In Study 2, where our request for subjects to explain to a ninth grader what certain evolutionary terms mean was at least an implicit request to discuss underlying evolutionary mechanisms, explanations involving characters were more common. Averaged across the evolved into/from and ancestor/descendant conditions, 55% of students mentioned characters in their explanations.

The Role of the Environment in Selection and Adaptation

Recognizing the importance of variation and of derived characters, however, is just the first step. Tree thinking also necessitates understanding the role of the environment in selecting the traits of individuals that eventually become the adaptations/characters we observe in species and higher taxa. We saw very little evidence of this type of thinking in our studies. In Study 1, references to the environment were so infrequent that that code was combined with several other codes in a catchall category of other evolutionary processes. Even for the horse diagram, which included graphics of characters defining particular taxa, only 33% of subjects referred to change, and only 22% referred to adaptation. In Study 2, only 31% of subjects mentioned the environment and 25% mentioned adaptation/selection. The only process code that was given more frequently was the vague notion of change (41% of subjects). It is clear that as educators we still have much to do to provide students with the concepts necessary to understand macroevolution.

A New Approach to Teaching Macroevolution

We suspect the poor performance of the university students in our studies reflects both the misleading nature of noncladogenic depictions of evolutionary relationships and the way that evolution is typically taught. Catley (2006, p. 768) argued that the reason students' understanding of macroevolution is so poor is that "microevolutionary mechanisms are taught almost exclusively in our schools, to the detriment of those mechanisms that allow us to understand the larger picture—macroevolution." Moreover, both students and their teachers have "virtually no understanding at all of the history of life on our planet." What little instruction undergraduates taking classes in the biological sciences do receive is unlikely to utilize a tree thinking approach (Baum et al., 2005; Catley, 2006; Sandvik, 2008). Goldsmith (2003) has shown, however, that despite initial problems with understanding, it is possible to teach cladistic thinking to biology undergraduates. Baum, Smith, and Donovan (2006) have gone a step further by suggesting a series of learning objectives when teaching tree thinking.

The results of Study 2 also have implications for how teachers and textbook authors should talk about evolutionary relationships. Many students are clearly prone to interpret the terms evolved into and evolved from as indicating an underlying anagenic process in which one taxon turned into another. Not only is this conception of species genesis spurious, it may be especially confusing when appearing in conjunction with cladograms, which correctly depict speciation as a cladogenic process involving branching events. Which interpretation should students favor, the one indicated by the verbal label or the one depicted in the diagram? Ideally, both linguistic and diagrammatic presentations of evolutionary relationships should be consistent with the correct, cladogenic understanding of macroevolution.

Concluding Remarks

Given that evolution is under attack in certain educational arenas, the National Academies of Science from 67 countries recently released a statement calling for "evidence-based" teaching of evolution in schools (The Academy of Sciences for the Developing World, 2006). It reads in part: "We, the undersigned Academies of Sciences, have learned that in various parts of the world, within science courses taught in certain public systems of education, scientific evidence, data, and testable theories about the origins and evolution of life on Earth are being concealed, denied, or confused with theories not testable by science. We urge decision makers, teachers, and parents to educate all children about the methods and discoveries of

science and to foster an understanding of the science of nature. Knowledge of the natural world in which they live empowers people to meet human needs and protect the planet.''

We hope this article has made a start in this direction by providing baseline data on students' interpretations of particular, and not very effective, evolutionary diagrams as well as of commonly used evolutionary terms. Further, we promote the use of scientifically appropriate diagrams—that is, cladograms/ phylogenetic trees—that (a) meet the criteria of evidenced-based reasoning, (b) fulfill the mandate in the National Science Education Standards to teach students to use the methodologies and tools from professional practice (American Association for the Advancement of Science, 2001; National Research Council, 1996), and (c) support, we hypothesize, clearer understanding of evolutionary processes.

Notes

[1]After answering the questions about the diagrams, subjects were asked whether they had taken biology in high school and whether they had taken each of seven college biology classes: biology today (nonmajors class), introduction to biological science A and B (the two semester introductory class for biology majors), evolution, principles of genetics, zoology, and ecology. Several students wrote in that they had taken human biology, a nonmajors class.

[2]Although classification issues involving the genus Homo are far from resolved, we use the term ''hominid'' throughout in this paper to refer to members of the genus Homo.

[3]The first set of questions asked students to interpret evolutionary relationships among taxa that were depicted in cladograms. The questions were very different from those asked in the present study. The second set of questions asked subjects to translate (redraw) relationships depicted in a nested hierarchical diagram in one format into an alternative but equivalent format. The final part of the booklet prior to the diagrams analyzed here was a set of true/false statements about evolution. If there was any crossover from the early diagrammatic reasoning tasks to the present one, it would be expected to lead to better performance than if the current tasks came first because subjects were exposed initially to appropriate evolutionary diagrams. Given the results of the present study, it is difficult to make the case that any such facilitation occurred. Moreover, in a more recent study in which subjects received both cladogenic and noncladogenic diagrams in a counterbalanced order, there was no effect of diagram order on subjects' responses.

[4]The first and third sets of questions asked students to interpret evolutionary relationships among taxa that were depicted in cladograms. The problems in the second part of the booklet required subjects to translate (redraw) relationships depicted in a nested hierarchical diagram in one format into an alternative but equivalent format. The final part of the booklet was a questionnaire asking students about their background in biology and about various concepts in evolution, including evolutionary deep time. All of the evolutionary diagrams subjects saw appropriately depicted evolution as a cladogenic process. Moreover, all subjects received exactly the same booklet of problems except for the bug question presented here.

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